

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/383,916DATE: 10/17/2000
TIME: 00:48:17

INPUT SET: S36012.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Anderson, Darrell R.
6
7 (ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
8 TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
9 PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
10 IMMUNOSUPPRESSANTS"
11
12 (iii) NUMBER OF SEQUENCES: 12
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
16 (B) STREET: 699 Prince Street
17 (C) CITY: Alexandria
18 (D) STATE: VA
19 (E) COUNTRY: USA
20 (F) ZIP: 22314
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 09/383,916
30 (B) FILING DATE: 26-AUG-1999
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/487,550
35 (B) FILING DATE: 07-JUN-1995
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Teskin, Robin L.
39 (B) REGISTRATION NUMBER: 35,030
40 (C) REFERENCE/DOCKET NUMBER: 012712-131
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 703-836-6620
44 (B) TELEFAX: 703-836-2021
45
46

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47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 705 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: Not Relevant

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: peptide

56

57

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

60 (B) LOCATION: 1..705

61

62 (ix) FEATURE:

63 (A) NAME/KEY: mat_peptide

64 (B) LOCATION: 1..705

65

66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68

69 ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA 48

70 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro

71 1 5 10 15

72

73 GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG 96

74 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val

75 20 25 30

76

77 TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA 144

78 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg

79 35 40 45

80

81 AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA 192

82 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile

83 50 55 60

84

85 CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA 240

86 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg

87 65 70 75 80

88

89 TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG 288

90 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly

91 85 90 95

92

93 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG 336

94 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg

95 100 105 110

96

97 GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA 384

98 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu

99 115 120 125

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100
101  GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT      432
102  Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
103      130                      135                      140
104
105  GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC      480
106  Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
107      145                      150                      155                      160
108
109  TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC      528
110  Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
111                      165                      170                      175
112
113  GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC      576
114  Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
115                      180                      185                      190
116
117  AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG      624
118  Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
119                      195                      200                      205
120
121  TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG      672
122  Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
123      210                      215                      220
124
125  GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA      705
126  Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *
127      225                      230                      235
128
129

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

```

133      (A) LENGTH: 234 amino acids
134      (B) TYPE: amino acid
135      (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

141  Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
142      1                      5                      10                      15
143
144  Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
145                      20                      25                      30
146
147  Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
148                      35                      40                      45
149
150  Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
151      50                      55                      60
152

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RAW SEQUENCE LISTING
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153 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
154 65 70 75 80
155
156 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
157 85 90 95
158
159 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
160 100 105 110
161
162 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
163 115 120 125
164
165 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
166 130 135 140
167
168 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
169 145 150 155 160
170
171 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
172 165 170 175
173
174 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
175 180 185 190
176
177 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
178 195 200 205
179
180 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
181 210 215 220
182
183 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
184 225 230 235
185

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 amino acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: Not Relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1431

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1431

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206      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
207
208      ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG      48
209      Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
210      1          5          10          15
211
212      GTC CTG TCC CAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG      96
213      Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
214      20          25          30
215
216      CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC      144
217      Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
218      35          40          45
219
220      AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA      192
221      Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
222      50          55          60
223
224      CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC      240
225      Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
226      65          70          75          80
227
228      AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG      288
229      Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
230      85          90          95
231
232      AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC      336
233      Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
234      100          105          110
235
236      GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT      384
237      Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
238      115          120          125
239
240      TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC      432
241      Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
242      130          135          140
243
244      TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC      480
245      Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
246      145          150          155          160
247
248      TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG      528
249      Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
250      165          170          175
251
252      GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG      576
253      Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
254      180          185          190
255
256      ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC      624
257      Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
258      195          200          205

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/383,916DATE: 10/17/2000
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Line	Error	Original Text
186	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO:3:
430	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO:5:
570	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO:7:
814	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO:9:
953	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO:11:
1195	Stop Codon at end of sequence removed - no error	